AMENDMENT TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.
What is claimed is:

1. (Currently amended) A method for identification of a ~~Gram positive~~ pathogenic Gram positive bacterium ~~organism~~ or a subset of pathogenic Gram positive bacteria ~~organisms being a member of~~ from a predetermined group of pathogenic Gram positive bacteria in a clinical sample comprising:

   a) providing ~~a~~ said clinical sample ~~specimen~~ containing at least partially purified nucleic acid,

   b) subjecting said clinical sample ~~specimen~~ to at least one amplification step and at least one detection step in one reaction vessel, said steps comprising:

      ba) ~~an amplification step using~~ at least one set of amplification primers capable of amplifying a pre-selected nucleic acid sequence comprising at least 20 nucleotides of the 16S/23S spacer region from a predetermined sub-group of pathogenic Gram positive bacteria to which said ~~Gram positive~~ pathogenic Gram positive bacterium or subset of pathogenic Gram positive bacteria ~~organism~~ belongs,

      bb) at least one internal control template, and

      ~~bb)~~ bc) ~~a detection step using~~ at least one hybridization reagent capable of detecting said pre-selected nucleic acid sequence ~~region~~ from said predetermined sub-group of pathogenic Gram positive bacteria, ~~said detection step bb)~~ further comprising:

         ~~bba)~~ bca) monitoring hybridization of said hybridization reagent at a pre-selected temperature, said hybridization being indicative for the presence in ~~the~~ said clinical sample of at least one species contained in said predetermined sub-group, and

         ~~bbb)~~ bcb) monitoring temperature dependence of hybridization, said temperature dependence being indicative for the presence of at least the

species of said pathogenic Gram positive bacterium or said subset of pathogenic Gram positive bacteria ~~organisms~~,

~~c)~~ wherein ~~identifying~~ said pathogenic Gram positive bacterium ~~organism~~ or said subset of pathogenic Gram positive bacteria ~~organisms~~ is identified based on the results of the monitoring steps in bca) and bcb). ~~bb).~~

2. (Currently amended) ~~A~~ The method according to claim 1, wherein said predetermined sub-group is a genus.

3. (Currently amended) ~~A~~ The method according to claim 1, wherein ~~the~~ said hybridization reagent comprises two probes complementary to adjacent sequences in said pre-selected ~~the target~~ nucleic acid sequence ~~region~~, one being labeled ~~labelled~~ by a ~~FRET~~ Fluorescence Resonance Energy Transfer (FRET) donor, and the other being labeled ~~labelled~~ by a FRET acceptor.

4. (Currently amended) ~~A~~ The method according to claim 1, wherein said predetermined group of pathogenic Gram positive bacteria comprises the species *Staphylococcus aureus* and *coagulase-negative staphococci.* ~~staphylococcus aureus and coagulase-negative staphococci.~~

5. (Currently amended) ~~A~~ The method according to claim 1, wherein ~~the~~ said predetermined sub-group comprises the species *Staphylococcus aureus, Streptococcus pneumoniae, Enterococcus faecium* and *Enterococcus faecalis.* ~~Staphylococcus aureus, Streptococcus pneumoniae, Enterococcus faecium and Enterococcus faecalis.~~

6. Cancelled.

7. Cancelled.

8. (Currently amended) ~~A~~ The method according to claim 1, wherein said species are selected from the genera *Staphylococcus, Enterococcus* and *Streptococcus*. ~~Staphylococcus, Enterococcus and Streptococcus~~.

9. (Currently amended) ~~A~~ The method according to claim 1, wherein said species are selected from the genus *Staphylococcus*. ~~Staphylococcus~~

10. (Currently amended) A kit for the identification of a ~~Gram positive~~ pathogenic Gram positive bacterium or a subset of pathogenic Gram positive bacteria selected from the genera *Enterococcus, Staphylococcus* and *Streptococcus* ~~Enterococcus, Staphylococcus and Streptococcus containing~~ a comprising:

a) at least one set of amplification primers capable of amplifying a pre-selected nucleic acid sequence comprising ~~of~~ at least 20 nucleotides of ~~from~~ the 16S/23S rRNA spacer region of ~~Enterococcus, Staphylococcus or Streptococcus.~~ *Enterococcus, Staphylococcus* or *Streptococcus,*

b) at least one internal control template, and

c) at least one hybridization reagent capable of detecting said pre-selected nucleic acid sequence,

wherein said amplifying and detecting are performed in one reaction vessel.